

matter was added. Claims 1-17 are pending. Applicants submit the amended and newly presented claims are supported by the specification.

For the reasons given below, Applicants submit the amended and newly presented claims are in condition for allowance and notification of that effect is earnestly solicited.

Petition for Extension of Time

It is noted that a two month petition for extension of time is necessary for provide for timeliness of the response. A request for such an extension is made extending the time for response from January 4, 2000 to March 4, 2000 (Saturday), thereby extending the date until Monday, March 6, 2000.

The Specification

The Examiner asserts that the specification includes trademarks, such as the acronym ELISA. Applicants believe that the term ELISA is an acronym that is not a trademark. Similarly, the application uses other abbreviations and acronyms that are believed to not be trademarks. If the Examiner provides evidence of a trademark employed in the present specification, Applicants will gladly amend the specification as appropriate.

Rejection of Claims Under § 112, First Paragraph

The Examiner rejected claims 1-16 under 35 U.S.C. § 112, first paragraph. The Examiner asserts that the specification does not enable the full scope of the claimed mutants of SPE-C. Applicants respectfully traverse this rejection.

The Examiner begins by correctly noting that the claims include SPE-C mutants obtained by deletion, substitution, or insertion of one or more amino acids, and that the specification does not specifically indicate each and every amino acid change that can be made in a SPE-C. The present application does, however, specifically teach that SPE-C includes only 235 amino acids. From this rather small protein, the specification teaches 39 specific amino acid residues that are preferred sites for mutations. The present specification also discloses 16 secondary structural features of SPE-C that are preferred regions in which amino acids can be mutated. The 16 secondary structural features include 5 beta strands, 6 loops, 1 beta barrel, 3 helices, and 1 groove (specification at page 11, line 12 through page 13). By describing these numerous discrete residues and specific structural features of the protein that are suitable for making mutations that